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SEQUENCE LISTING

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DEN DIJKE, Peter

<120> PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS, CORRESPONDING  
NUCLEIC ACID MOLECULES AND THEIR USE

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<141> 1999-03-12

<150> PCT/GB93/02367

<151> 1993-11-17

<150> US 09/039,177

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58

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59

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 Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln  
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 Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp  
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 Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly  
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 Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val  
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 Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu  
 225 230 235 240  
 Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu  
 245 250 255  
 Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn  
 260 265 270  
 Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly  
 275 280 285  
 Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met  
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60

Q

Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met  
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Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu  
325 330 335

Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala  
340 345 350

Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp  
355 360 365

Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu  
370 375 380

Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys  
385 390 395 400

Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg  
405 410 415

Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp  
420 425 430

Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys  
435 440 445

Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu  
450 455 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn  
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Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln  
485 490 495

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61

2

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62

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<400> 10

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 35 40 45

Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu Thr Thr Asp Lys  
 50 55 60

Val Ile His Asn Ser Met Cys Ile Ala Glu Ile Asp Leu Ile Pro Arg  
 65 70 75 80

Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys Thr Gly Ser Val Thr  
 85 90 95

Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn Lys Ile Glu Leu Pro  
 100 105 110

Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro Val Glu Leu Ala Ala  
 115 120 125

Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile Ser Leu Met Leu Met  
 130 135 140

Val Tyr Ile Cys His Asn Arg Thr Val Ile His His Arg Val Pro Asn  
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Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile Ser Glu Gly Thr Thr  
 165 170 175

Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser Gly Ser Gly Ser Gly  
180 185 190

Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg Thr Ile Val Leu Gln  
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Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly Lys Trp  
210 215 220

Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser Ser Arg Glu Glu Arg  
225 230 235 240

Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu Arg His  
245 250 255

Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn Gly Thr  
260 265 270

Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly Ser Leu  
275 280 285

Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val Glu Gly Met Ile Lys  
290 295 300

Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His Leu His Met Glu Ile  
305 310 315 320

Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser  
325 330 335

Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu  
340 345 350

Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp Thr Ile Asp Ile Ala  
355 360 365

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu  
370 375 380

Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp  
385 390 395 400

Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser  
405 410 415

Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val  
420 425 430

Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln  
 435 440 445

Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu  
 450 455 460

Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala  
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Gln Gln Glu Gly Ile Lys Met  
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 <212> DNA  
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<210> 12  
 <211> 502  
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<400> 12

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Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser  
 35 40 45

Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val  
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Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro  
 65 70 75 80

Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His  
 85 90 95

66

4

Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro  
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Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu  
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Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg  
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Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser  
145 150 155 160

Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe  
165 170 175

Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu  
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Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly  
195 200 205

Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser  
210 215 220

Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg  
225 230 235 240

Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu  
245 250 255

Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu  
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Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu  
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Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser  
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Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln  
305 310 315 320

Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu  
325 330 335

Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val  
340 345 350

67

C

Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg  
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Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile  
 370 375 380

Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe  
 385 390 395 400

Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile  
 405 410 415

Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro  
 420 425 430

Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro  
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Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala  
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Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr  
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Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu  
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Lys Pro Lys Val Ile His  
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 <211> 2070  
 <212> DNA  
 <213> Mus musculus

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<211> 532  
<212> PRT  
<213> Mus musculus

<400> 14

Met Thr Gln Leu Tyr Thr Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe

1

5

10

15

Ile Ile Ser His Val Gln Gly Gln Asn Leu Asp Ser Met Leu His Gly  
20 25 30

Thr Gly Met Lys Ser Asp Leu Asp Gln Lys Lys Pro Glu Asn Gly Val  
35 40 45

Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser  
50 55 60

Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly  
65 70 75 80

His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu  
85 90 95

Thr Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp  
100 105 110

Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn  
115 120 125

Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val Ile Gly  
130 135 140

Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Val Leu Ile Ser Met  
145 150 155 160

Ala Val Cys Ile Val Ala Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr  
165 170 175

Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp  
180 185 190

Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu Lys Asp  
195 200 205

Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu  
210 215 220

Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val  
225 230 235 240

Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu  
245 250 255



Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe  
260 265 270

Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile  
275 280 285

Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln  
290 295 300

Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe  
305 310 315 320

Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr  
325 330 335

Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr  
340 345 350

Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile  
355 360 365

Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala  
370 375 380

Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Ile Pro Leu Asn Thr  
385 390 395 400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
405 410 415

Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
420 425 430

Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
435 440 445

Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
450 455 460

Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg  
465 470 475 480

Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val  
485 490 495

Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu  
500 505 510

71

Q

Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln  
 515 520 525

Asp Val Lys Ile  
 530

<210> 15  
 <211> 2160  
 <212> DNA  
 <213> Mus musculus

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 agctgcctac agaccaacta cacctgtgag acagatgggg cttgcatggg ctccatcttt 180  
 aacctggatg gcgtggagca ccatgtacgt acctgcatcc ccaaggtgga gctggttcct 240  
 gctggaaagc ctttctactg cctgagttca gaggatctgc gcaacacaca ctgctgctat 300  
 attgacttct gcaacaagat tgacctcagg gtccccagcg gacacctcaa ggagcctgcg 360  
 caccctcca tgtggggccc tgtggagctg gtcggcatca tcgccggccc cgtcttcctc 420  
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 aaccgccaga ggttggacat ggaggacccc tcttgcgaga tgtgtctctc caaagacaag 540  
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 aactggtggc agagttatga ggccttgcca gtgatgggaa agatgatgcg ggagtgtctg 1440

tacgccaatg gtgctgcccg tctgacagct ctgcgcatca agaagactct gtcccagcta 1500  
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 gtgaggatga ctgcagccac cgtgcaagcg tcgtggaggc ctatcctctt gtttctgccc 1620  
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 gaggaaccgg aagtttctcc ctcttccc tagcagtcct gagccacacc atccttctca 1980  
 tggacatccg gaggactgcc cctagagaca caacctgctg cctgtctgtc cagccaagtg 2040  
 cgcattgtcc gaggtgtgtc ccacattgtg cctgggtctgt gccacgccg tgtgtgtgtg 2100  
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<210> 16  
 <211> 505  
 <212> PRT  
 <213> Mus musculus

<400> 16

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1 5 10 15

Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu  
20 25 30

Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr  
35 40 45

Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His  
50 55 60

His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys  
65 70 75 80

Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys  
85 90 95

Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His  
100 105 110

Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val  
115 120 125

Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile  
130 135 140

Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln  
145 150 155 160

Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp  
165 170 175

Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly  
180 185 190

Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val  
195 200 205

Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly  
210 215 220

Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu  
225 230 235 240

Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu  
245 250 255

Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn  
260 265 270

Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly  
275 280 285

Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met  
290 295 300

Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met  
305 310 315 320

Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu  
325 330 335

Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala  
340 345 350

Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp  
355 360 365

Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu  
370 375 380

Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys  
385 390 395 400

Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg  
405 410 415

Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp  
420 425 430

Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys  
435 440 445

Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln Ser Tyr Glu  
450 455 460

Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn  
465 470 475 480

Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln  
485 490 495

Leu Ser Val Gln Glu Asp Val Lys Ile  
500 505

<210> 17  
<211> 1952  
<212> DNA  
<213> Mus musculus

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tggggaagcgg cggcgggtta acttcggctg aatcacaacc atttggcgt gagctatgac 120  
aagagagcaa acaaaaagtt aaaggagcaa cccggccata agtgaagaga gaagtttatt 180  
gataacatgc tcttacgaag ctctggaaaa ttaaattgtg gcaccaagaa ggaggatgga 240  
gagagtacag cccccacccc tcggcccaag atcctacgtt gtaaattgcca ccaccactgt 300  
ccggaagact cagtcaacaa tatctgcagc acagatgggt actgcttcac gatgatagaa 360  
gaagatgact ctggaatgcc tgttgtcacc tctggatgtc taggactaga agggtcagat 420  
tttcaatgtc gtgacactcc cattcctcat caaagaagat caattgaatg ctgcacagaa 480  
aggaatgagt gtaataaaga cctccacccc actctgcctc ctctcaagga cagagatttt 540  
gttgatgggc ccatacacca caaggccttg cttatctctg tgactgtctg tagtttactc 600  
ttggtcctca ttattttatt ctgttacttc aggtataaaa gacaagaagc ccgacctcgg 660  
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ttgatcgagc agtctcagag ctcgggaagt ggatcaggcc tccctctgct ggtccaaagg 780  
 acaatagcta agcaaattca gatggtgaag cagattggaa aaggccgcta tggcgaggtg 840  
 tggatgggaa agtggcgtgg agaaaagggtg gctgtgaaag tgttcttcac cacggaggaa 900  
 gccagctggt tccgagagac tgagatatat cagacgggtcc tgatgcggca tgagaatatt 960  
 ctgggggttca ttgctgcaga tatcaaaggg actgggtcct ggactcagtt gtacctcatc 1020  
 acagactatc atgaaaacgg ctccctttat gactatctga aatccaccac cttagacgca 1080  
 aagtccatgc tgaagctagc ctactcctct gtcagcggcc tatgccattt acacacggaa 1140  
 atcttttagca ctcaaggcaa gccagcaatc gccatcgag acttgaaaag taaaaacatc 1200  
 ctggtgaaga aaaatggaac ttgctgcata gcagacctgg gcttggctgt caagttcatt 1260  
 agtgacacaa atgaggttga catccccacc aacacccggg ttggcaccaa gcgctatatg 1320  
 cctccagaag tgctggacga gagcttgaat agaaaccatt tccagtccta cattatggct 1380  
 gacatgtaca gctttggact catcctctgg gagattgcaa ggagatgtgt ttctggaggt 1440  
 atagtggaaag aataccagct tccctatcac gacctgggtgc ccagtgacct ttcttatgag 1500  
 gacatgagag aaattgtgtg catgaagaag ttacggcctt cattcccaa tcgatggagc 1560  
 agtgatgagt gtctcaggca gatggggaag cttatgacag agtgctgggc gcagaatcct 1620  
 gcctccaggc tgacggccct gagagttaag aaaacccttg ccaaaatgtc agagtcccag 1680  
 gacattaaac tctgacgtca gatacttgtg gacagagcaa gaatttcaca gaagcatcgt 1740  
 tagcccaagc cttgaacgtt agcctactgc ccagtgagtt cagactttcc tggaagagag 1800  
 cacggtgggc agacacagag gaaccagaa acacggattc atcatggctt tctgaggagg 1860  
 agaaactgtt tgggtaactt gttcaagata tgatgcatgt tgctttctaa gaaagccctg 1920  
 tattttgaat taccattttt ttataaaaaa aa 1952

<210> 18  
 <211> 502  
 <212> PRT  
 <213> Mus musculus

<400> 18

Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys Lys Glu  
1 5 10 15

Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu Arg Cys  
20 25 30

Lys Cys His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser  
35 40 45

76

J

Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Met  
50 55 60

Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln  
65 70 75 80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys  
85 90 95

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro  
100 105 110

Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys Ala Leu  
115 120 125

Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu  
130 135 140

Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg Tyr Ser  
145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu  
165 170 175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu  
180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys  
195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg  
210 215 220

Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser  
225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu  
245 250 255

Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp  
260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr  
275 280 285

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu  
290 295 300

32  
cont

7

4

Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe  
305 310 315 320

Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys  
325 330 335

Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly  
340 345 350

Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro  
355 360 365

Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp  
370 375 380

Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met  
385 390 395 400

Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys Val Ser  
405 410 415

Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro  
420 425 430

Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met Lys Lys  
435 440 445

Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg  
450 455 460

Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro Ala Ser  
465 470 475 480

Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met Ser Glu  
485 490 495

Ser Gln Asp Ile Lys Leu  
500

<210> 19  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Sense primer, extracellular domain.

<220>

28

4



<221> misc\_feature  
 <222> (20)..(20)  
 <223> The nucleotide at position 20 may be any nucleotide

<400> 19  
 gcggatcctg ttgtgaaggn aatatgtg 28

<210> 20  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sense primer, kinase domain II

<400> 20  
 gcgatccgtc gcagtcaaaa tttt 24

<210> 21  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Sense Primer, Kinase domain VIB

<400> 21  
 gcggatccgc gatatatataa aagcaa 26

<210> 22  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Anti-sense primer, Kinase Domain VIB

<400> 22  
 cggaattctg gtgcatata 20

<210> 23  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide probe

<400> 23  
 attcaagggc acatcaactt catttgtgtc actgttg 37

<210> 24  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' oligonucleotide primer

<400> 24  
gcg gatccac catggcggag tcggcc

26

<210> 25  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> 3' oligonucleotide primer

<400> 25  
aacaccgggc cggcgatgat

20

<210> 26  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence in Subdomain I

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> Xaa at position 2 may be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (4)..(5)  
<223> Xaa at position 4 and 5 may be any amino acid

<400> 26  
Gly Xaa Gly Xaa Xaa Gly  
1 5

<210> 27  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 27  
Asp Phe Lys Ser Arg Asn  
1 5

<210> 28  
<211> 6  
<212> PRT  
<213> Homo sapiens

<400> 28  
Asp Leu Lys Ser Lys Asn  
1 5

80

4

<210> 29  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 29

Gly Thr Lys Arg Tyr Met  
 1 5

<210> 30  
 <211> 182  
 <212> PRT  
 <213> Homo sapiens

<400> 30

Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala Glu Val Tyr Lys Ala  
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Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu Thr Val Ala Val Lys  
 20 25 30

Ile Phe Pro Tyr Asp His Tyr Ala Ser Trp Lys Asp Arg Lys Asp Ile  
 35 40 45

Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile Leu Gln Phe Leu Thr  
 50 55 60

Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln Tyr Trp Leu Ile Thr  
 65 70 75 80

Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr Leu Thr Arg His Val  
 85 90 95

Ile Ser Trp Glu Asp Leu Arg Asn Val Gly Ser Ser Leu Ala Arg Gly  
 100 105 110

Leu Ser His Leu His Ser Asp His Thr Pro Cys Gly Arg Pro Lys Met  
 115 120 125

Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn Ile Leu Val Lys Asn  
 130 135 140

Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu Ser Leu Arg Leu Gly  
 145 150 155 160

Pro Tyr Ser Ser Val Asp Asp Leu Ala Asn Ser Gly Gln Val Gly Thr  
 165 170 175

21

d

Ala Arg Tyr Met Ala Pro  
180

<210> 31  
<211> 176  
<212> PRT  
<213> Mus musculus

<400> 31

Leu Leu Glu Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala  
1 5 10 15

Gln Leu Met Asn Asp Phe Val Ala Val Lys Ile Phe Pro Leu Gln Asp  
20 25 30

Lys Gln Ser Trp Gln Ser Glu Arg Glu Ile Phe Ser Thr Pro Gly Met  
35 40 45

Lys His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser  
50 55 60

Asn Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly  
65 70 75 80

Ser Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu  
85 90 95

Cys His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu  
100 105 110

Asp Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His  
115 120 125

Arg Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala  
130 135 140

Val Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro  
145 150 155 160

Pro Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
165 170 175

<210> 32  
<211> 175  
<212> PRT  
<213> Mus musculus

<400> 32

Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala  
Page 36

32

Q

1 5 15

Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp  
20 25 30

Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met  
35 40 45

Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr  
50 55 60

Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly  
65 70 75 80

Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu  
85 90 95

Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu  
100 105 110

Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg  
115 120 125

Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys  
130 135 140

Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala  
145 150 155 160

Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
165 170 175

<210> 33  
<211> 178  
<212> PRT  
<213> Caenorhabditis elegans

<400> 33

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly  
1 5 10 15

Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Leu Asp  
20 25 30

Glu Pro Ala Phe His Lys Glu Thr Glu Ile Phe Glu Thr Arg Met Leu  
35 40 45

Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr  
Page 37

23

Q

50

55

Gly Phe Val Thr Glu Leu Trp Leu Val Thr Glu Tyr His Pro Ser Gly  
65 70 75 80

Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr  
85 90 95

Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn  
100 105 110

Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg  
115 120 125

Asp Ile Lys Ser Lys Asn Ile Met Val Lys Asn Asp Leu Thr Cys Ala  
130 135 140

Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser  
145 150 155 160

Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu  
165 170 175

Ala Pro

<210> 34  
<211> 513  
<212> PRT  
<213> Mus musculus

<400> 34

Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys  
1 5 10 15

Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe  
20 25 30

Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu  
35 40 45

Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp  
50 55 60

Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu  
65 70 75 80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp

84

8

Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu  
100 105 110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn  
115 120 125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu  
130 135 140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val  
145 150 155 160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln  
165 170 175

Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu  
180 185 190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys  
195 200 205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln  
210 215 220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly  
225 230 235 240

Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly  
245 250 255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys  
260 265 270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu  
275 280 285

Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His  
290 295 300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His  
305 310 315 320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala  
325 330 335

75

1

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser  
340 345 350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro  
355 360 365

Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg  
370 375 380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg  
385 390 395 400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu  
405 410 415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val  
420 425 430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His  
435 440 445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His  
450 455 460

Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr  
465 470 475 480

Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr  
485 490 495

Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser  
500 505 510

Leu

<210> 35  
<211> 536  
<212> PRT  
<213> Mus musculus

<400> 35

Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys  
1 5 10 15

Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr  
20 25 30

76

21



Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg  
35 40 45

Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg  
50 55 60

Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp  
65 70 75 80

Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn  
85 90 95

Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg  
100 105 110

Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro  
115 120 125

Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu  
130 135 140

Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr  
145 150 155 160

Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg  
165 170 175

Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe  
180 185 190

Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu  
195 200 205

Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg  
210 215 220

Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val  
225 230 235 240

Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu  
245 250 255

Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile  
260 265 270

Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile  
275 280 285

32  
Cont

87

1

Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn  
290 295 300

Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg  
305 310 315 320

Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly  
325 330 335

His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu  
340 345 350

Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val  
355 360 365

Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly  
370 375 380

Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe  
385 390 395 400

Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val  
405 410 415

Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp  
420 425 430

Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu  
435 440 445

Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile  
450 455 460

Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr  
465 470 475 480

Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly  
485 490 495

Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr  
500 505 510

Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp  
515 520 525

Leu Leu Pro Lys Glu Ser Ser Ile  
530 535

<210> 36  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 36

Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val Leu  
 1 5 10 15

Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys Ser Val  
 20 25 30

Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val Lys Phe Pro  
 35 40 45

Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr Cys Asp Asn Gln  
 50 55 60

Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser Ile Cys Glu Lys Pro  
 65 70 75 80

Gln Glu Val Cys Val Ala Val Trp Arg Lys Asn Asp Glu Asn Ile Thr  
 85 90 95

Leu Glu Thr Val Cys His Asp Pro Lys Leu Pro Tyr His Asp Phe Ile  
 100 105 110

Leu Glu Asp Ala Ala Ser Pro Lys Cys Ile Met Lys Glu Lys Lys Lys  
 115 120 125

Pro Gly Glu Thr Phe Phe Met Cys Ser Cys Ser Ser Asp Glu Cys Asn  
 130 135 140

Asp Asn Ile Ile Phe Ser Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu  
 145 150 155 160

Leu Leu Val Ile Phe Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu  
 165 170 175

Gly Val Ala Ile Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn  
 180 185 190

Arg Gln Gln Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys  
 195 200 205

Leu Met Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg  
 210 215 220

32  
 cont

34

Ser Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu  
225 230 235 240

Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe Ala  
245 250 255

Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln Phe Glu  
260 265 270

Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala Ser Trp Lys  
275 280 285

Thr Glu Lys Asp Ile Phe Ser Asp Ile Asn Leu Lys His Glu Asn Ile  
290 295 300

Leu Gln Phe Leu Thr Ala Glu Glu Arg Lys Thr Glu Leu Gly Lys Gln  
305 310 315 320

Tyr Trp Leu Ile Thr Ala Phe His Ala Lys Gly Asn Leu Gln Glu Tyr  
325 330 335

Leu Thr Arg His Val Ile Ser Trp Glu Asp Leu Arg Lys Leu Gly Ser  
340 345 350

Ser Leu Ala Arg Gly Ile Ala His Leu His Ser Asp His Thr Pro Cys  
355 360 365

Gly Arg Pro Lys Met Pro Ile Val His Arg Asp Leu Lys Ser Ser Asn  
370 375 380

Ile Leu Val Lys Asn Asp Leu Thr Cys Cys Leu Cys Asp Phe Gly Leu  
385 390 395 400

Ser Leu Arg Leu Asp Pro Thr Leu Ser Val Asp Asp Leu Ala Asn Ser  
405 410 415

Gly Gln Val Gly Thr Ala Arg Tyr Met Ala Pro Glu Val Leu Glu Ser  
420 425 430

Arg Met Asn Leu Glu Asn Ala Glu Ser Phe Lys Gln Thr Asp Val Tyr  
435 440 445

Ser Met Ala Leu Val Leu Trp Glu Met Thr Ser Arg Cys Asn Ala Val  
450 455 460

Gly Glu Val Lys Asp Tyr Glu Pro Pro Phe Gly Ser Lys Val Arg Glu  
Page 44

y2  
Cont

91

<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Serine/threonine kinase consensus

<400> 38

Asp Leu Lys Pro Glu Asn  
1 5

<210> 39  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tyrosine kinase consensus

<400> 39

Asp Leu Ala Ala Arg Asn  
1 5

<210> 40  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Act R-II motif

<400> 40

Asp Ile Lys Ser Lys Asn  
1 5

<210> 41  
<211> 6  
<212> PRT  
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<220>  
<223> Act R-IIB motif

<400> 41

Asp Phe Lys Ser Lys Asn  
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<210> 42  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> TBR-II motif

<400> 42

Asp Leu Lys Ser Ser Asn  
1 5

<210> 43

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial Peptide

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is Thr or Ser

<220>

<221> MISC\_FEATURE

<222> (3)..(4)

<223> Xaa at position three and four can be any amino acid

<220>

<221> MISC\_FEATURE

<222> (5)..(5)

<223> Xaa at position five is Tyr or Phe

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Xaa at position six may be any amino acid

<400> 43

Gly Xaa Xaa Xaa Xaa Xaa  
1 5

<210> 44

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> MISC\_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is any amino acid

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is Ile or Val

<220>

<221> MISC\_FEATURE

<222> (4)..(4)

f2  
Ant

93

1

<223> Xaa at position 4 is Lys or Arg

<220>

<221> MISC\_FEATURE

<222> (6)..(6)

<223> Xaa at position 6 is Thr or Met.

<400> 44

Xaa Pro Xaa Xaa Trp Xaa  
1 5

<210> 45

<211> 6

<212> PRT

<213> Homo sapiens

<400> 45

Gly Thr Arg Arg Tyr Met  
1 5

<210> 46

<211> 6

<212> PRT

<213> Homo sapiens

<400> 46

Gly Thr Ala Arg Tyr Met  
1 5

94

Q